FIG. 1

```
atgttagccaacagctcctcaaccaacagttctgttctcccgtgtcctgactaccgacct
acccaccgcctgcacttggtggtctacagcttggtgctggctgccgggctccccctcaac
gcgctagccctctgggtcttcctgcgcgcgctgcgcgtgcactcggtggtgagcgtgtac
atgtgtaacctggcggccagcgacctgctcttcaccctctcgctgcccgttcgtctctcc
tactacgcactgcaccactggcccttccccgacctcctgtgccagacgacgggcgccatc
ttccagatgaacatgtacggcagctgcatcttcctgatgctcatcaacgtggaccgctac
gccgccatcgtgcacccgctgcgactgcgccacctgcggcggccccgcgtggcgcggctg
ctctgcctgggcgtgtgggcgctcatcctggtgtttgccgtgcccgccgcccgcgtgcac
aggccctcgcgttgccgctaccgggacctcgaggtgcgcctatgcttcgagagcttcagc
gacgagctgtggaaaggcaggctgctgcccctcgtgctgctggccgaggcgctgggcttc
ctgctgcccctggcggcggtggtctactcgtcgggccgagtcttctggacgctggcgcgc
cccgacgccacgcagagccagcggcggcggaagaccgtgcgcctcctgctggctaacctc
gtcatcttcctgctgtgcttcgtgccctacaacagcacgctggcggtctacgggctgctg
cggagcaagctggtggcggccagcgtgcctgcccgcgatcgcgtgcgcggggtgctgatg
gtgatggtgctgctggccggcgccaactgcgtgctggacccgctggtgtactactttagc
gccgagggcttccgcaacaccctgcgcggcctgggcactccgcaccgggccaggacctcg
gccaccaacgggacgcgggcggcgctcgcgcaatccgaaaggtccgccgtcaccaccgac
gccaccaggccggatgccgccagtcaggggctgctccgaccctccgactcccactctctg
tcttccttcacacagtgtccccaggattccgccctctga
```

FIG. 2

```
MLANSSSTNSSVLPCPDYRPTHRLHLVVYSLVLAAGLPLNALALWVFLRALRVHSVVSVY
MCNLAASDLLFTLSLPVRLSYYALHHWPFPDLLCQTTGAIFQMNMYGSCIFLMLINVDRY
AAIVHPLRLRHLRRPRVARLLCLGVWALILVFAVPAARVHRPSRCRYRDLEVRLCFESFS
DELWKGRLLPLVLLAEALGFLLPLAAVVYSSGRVFWTLARPDATQSQRRRKTVRLLLANL
VIFLLCFVPYNSTLAVYGLLRSKLVAASVPARDRVRGVLMVMVLLAGANCVLDPLVYYFS
AEGFRNTLRGLGTPHRARTSATNGTRAALAQSERSAVTTDATRPDAASQGLLRPSDSHSL
SSFTQCPQDSAL
```

FIG. 3A

gcgtccgaaaaaaaaagaaattcctttacatactacaacatgaatagatcttggaaacat
tatgctaagtgaaataaaccagacacaaaaggacaaatattgtatgattccactcatatg
aggtatctagaataggcaaattcattgagacagaaagtagactagaaccagaagctgaat
ggggtgcggtgggtagtactgcttaatgactgcagagttgttgcttggttgatgaaaaag
ttctatttctggaaacagagagtggtgacggttaagcaacactgtcttggtctttttgt
tgttgttgttgtttttgagacggactctcactctgtctcccaggccggagtgcgatggat
tagacctgctaggggagcacttggcaaaactcaacccacagggccttcccctgcctagca
agactgtgctgtcaaatttattcacatgtggctctggtcaagactagcatgcaatcagcc
tatgagggcattattatattattattcccattttacagatgaagaaactgagaagtcaaa
ccattaagctgaacccagtttgctttgaccacaaatccagccctcacaggcgcagtgatg
catgtgatgcgtaaggctgggatgttgttctgtatttgggagttttgtttgcttgtttgc
ttgtctgacatggagtctcactctgtcacccaggctggagtgcagtggcgtgatctcggc
tcactgcaacctccgcctcccgggttcaaggactctcctgctgcagcctcccatgtactc
aaagagtttgacctttattctttggataatgaggagctagcctagcacctggtccaagga
ggtgctccataagaccacctattgatttgtgcttattatctgtctccctccaatggaatg
taaaggaggtgggggcaaagacttttgctttgttccctgctgtgaacatgcctggaact
ttctatgagctcagtaagcaaggaaagaaggaaggaagagatcttgagatagtaacagca
acctaagcgttttacacacgtcatcttaatctccaaacctcatgaattctctctctctct
ctctcatttttgagacagagtctcgctctgtcacccaggctggagtgcagtggcgtgat
ctcgactcattgcaacctctgcctcctggattcaatcaattctcatgccttagcctactg
aggagctgggattacaagtgcacgccaccatacccggctaatctttgtatttttagtaga
ggcaagattttgtcatgttggccaggttggtcttcaactcctggcctcaagtaatccacc
cacatcagcctcccaaagtgctgagatcacaggcatgaggtaccatgcagccgccttttt
ttttttttttgagatggagtctcgttttgttacccaggctggagggcagtggtacgatgt
cagctcactgcaacctccgcctcctgggttcaagtgattctcctgtgtgagcctcctgag
tagctgggactacaggtgcatgccaccacatctggctaatttttgtatttttagtagaga
cagggttttgccaggttggccaggctgatctcgaactcctgacctcaggtgatctgcccg
cctcagtctcccaaagtgctggattacaggtgtgggccactacgccggccctggccctct
ttctttctttttgagatgggctcactctgtcacccaggcaggagtgcagtggtgggctt
gaggctcactgcactgcagcctccacctccctggagtcaagtgattctctcacctcagcc
tcacaagtagctgggactacgggcatgtgccacaatgcctggctaatttttaatttttt
aatatttttatttttatttttttttgagacagagtcttgctctgtcacccaggccggagt
gcaatggtgtgatctcggctcactgcaacctctgctcaagcaattctccctgccttagcc
tcctgagtagctgggattacaggcgcctgccaccacgcccggctaatttttttttttttt
tagtagagacaggattttgccatgttggccaggatggtctcaacctcctgacctcaggtg
atccgcccacctcagcctcccaaagtgctcggattacagatgtgagccaccacgcccagc
cttatttttatttttttatttttatttttatttatttattttgagatggagtttcactcttgt
tgcccaggctggagtgcaatggcgcgatcttggctcactgcaaactccacccccaggtt
caagcaattctcctgtctcagccccctgagtagctgggattacaggcgcccgccctatg
ccaggctaatttttggtatttttttttagtagagatggggtttcaccatgttggccaagct
ggtctcgaactcctgacctcaggtgatccacctgcctcggcctcccaaagtgctgggatt
acaggcgtgagccaccgcgcctggctatttttatttttttgagacagagtttcacttttgt
tgtccaggctggagtgcaatggcacagtctcagctcactgcaacctctgcctcctggttt
caagcgattctcctgtctcagcctcccgagtagctgggattacaggcgtgcaccaccacg
cccagctaatttttgtatttttagtagagatggggtttcaccatattggacaggttggtc
tcgaactcctgacctcaggtaatccacccgcctcggcctcccaaaatgctgggattacag

FIG. 3B

gtgtgagccactgcacctggccctgtatttttttgtagagatggggtttcgccgtgttgc
ccaggctggtccccaactcctaggttcaagcaattggtctgccttggcctcccaaagtgc
caggattacaggtgtaagccattgcacccagccaagattaatttttttgaagtcacacaa
ctaggcaagttagcaaaaccaagatttaaacctaggcatccgagtccctgccttcaaacc
tgggtgtttaacactatactatatagtcctgccgtaggaacctattctagcccaatggca
gacttgaggctgagaaaagattcagaaggcctgccagtggagctaaacatttgtgtgtgc
agccctgtctctgtataacttccggcttgccttcctattccaggtctctgctgctgatga
agctgtgaccaaacgcacccaacccttggcagccatctgtccctgcagccatagcccaca
ttcccatgacctccctctgcttgttttgggaccatgtctgtacagcctctaggccccagc
cccggaggtgaatgccatgccatgattctggtgtgctccatggcatccccagcctagctc
ccaatcccactttggcacg

FIG. 4

ACACACATGCCATTGCGCTGTCCGTGCCCGACTCCCAACGCCTCTCGTTCTGGGAGGCTT
ACAGGGTGTACACACAAGAAGGTGGGCTGGGCACTTGGACCTTTGGGTGGCAATTCCAGC
TTAGCAACGCAGAAGAGTACAAAGTGTGGAAGCCAGGGCCCAGGGAAGGCAGTGCTGCTG
GAAATGGCTTCTTTAAACTGTGAGCACGCAGAGCACCCCTTCTCCAGCGGTGGGAAGTGA
TGCAGAGAGCCCACCCGTGCAGAGGGCAGAAGAGGACGAAATGCCTTTGGGTGGGCAGGG
CATTAAACTGCTAAAAGCTGGTTAGATGGAACAGAAAATGGGCATTCTGGATCTAAACCG
CCACAGGGGCCTGAGAGCTGAAGAGCACCAGGTTTGGTGGACAAAGCTACTGAGATGCCT
GTTCATCTGCTGACTTCTGTCTAGGCTCATGGATGCCACCCCCTTTCATTTCGGCCTAGG
CTTCCCCTGCTCACCACTGAGGCCTAATACAAGAGTTCCTATGGACAGAACTACATTCTT
TCTCGCATAGTGACTTGTGACAATTTAGACTTGGCATCCAGCATGGGATAGTTGGGGCAA
GGCAAAACTAACTTAGAGTTTCCCCCTCAACAACATCCAAGTCCAAACCCTTTTTAGGTT
ATCCTTTCTTCCATCACATCCCCTTTTCCAGGCCTCCTCCATTTTAGGTCCTTAATATTC
TTTCTTTTTCTCTCTCTCTCGTTTCTCTCTTCTCTCTCCTCTCCTCTCTCTTCTCCTCTT
CTCTCTCTCTCCCTCTCTCCTTTGTCCAGAGTAAGGATAAAATTCTTTCTACTAAAGCAC
TGGTTCTCAAACTTTTTGGTCTCAGACCCCACTCTTAGAAATTGAGGATCTCAAAGAGCT
TTGCTTATATTTTGTTCTTTTGATACTTACCATACTAGAAATTAAAGCGAATACATTTTT
AAAATAAATACACATGCACACATTACATTAGCCATGGGAGCAATAATGTCACCACACACA
CTTCATGAAGCCTCTGGAAAACTCTACAGTATACTTGTGAGAGAATGAGAGTGAAAGGGA
CAAATAACATCTGTGTAGCAGTATTATGAAAATAGCTTGACCTCGTGGACTTCCTCAGAG
GGTTGGTCCCTGGATCACACTTTGAGAACCATACTTGTCCTGAAGTATTGGAGTTCATGT
CTAACTTCTTCCCAGGGCATTATGTACAGTGCTTTTTATTACTGTGGGGAGAGGGCAGTG
CTAAATAAATTAATCACTACTGATAAAAAAAAAAAAAAAAG

FIG. 5

MLANSSSTNS SVLPCPDYRP THR**LHLVVYS LVLAAGLPLN ALALWVFL**RA
LRVHSVVS**VY MCNLAASDLL FTLSLPVRLS YYAL**HHWPFP DLLCQTTG**AI**
FQMNMYGSCI FLMLINVDRY AAIVHPLRLR HLRRPR**VARL LCLGVWALIL**
VFAVPAARVH RPSRCRYRDL EVRLCFESFS DELWKGRLLP **LVLLAEALGF**
LLPLAAVVYS SGRVFWTLAR PDATQSQRRR KTVRL**LLANL VIFLLCFVPY**
NSTLAVYGLL RSKLVAASVP ARDRVR**GVLM VMVLLAGANC VLDPLVYYFS**
AEGFRNTLRG LGTPHRARTS ATNGTRAALA QSERSAVTTD ATRPDAASQG
LLRPSDSHSL SSFTQCPQDS AL

FIG. 6A

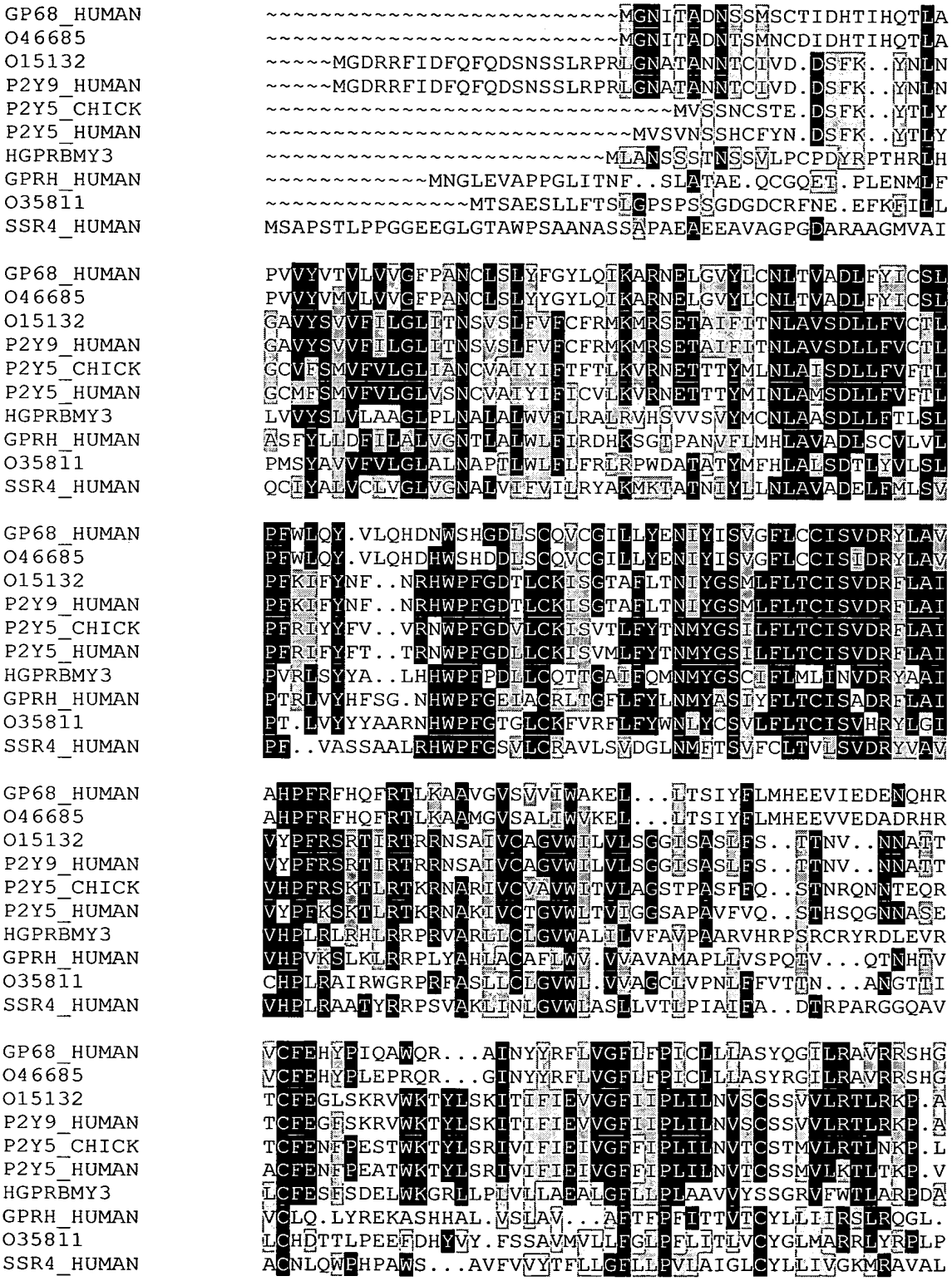
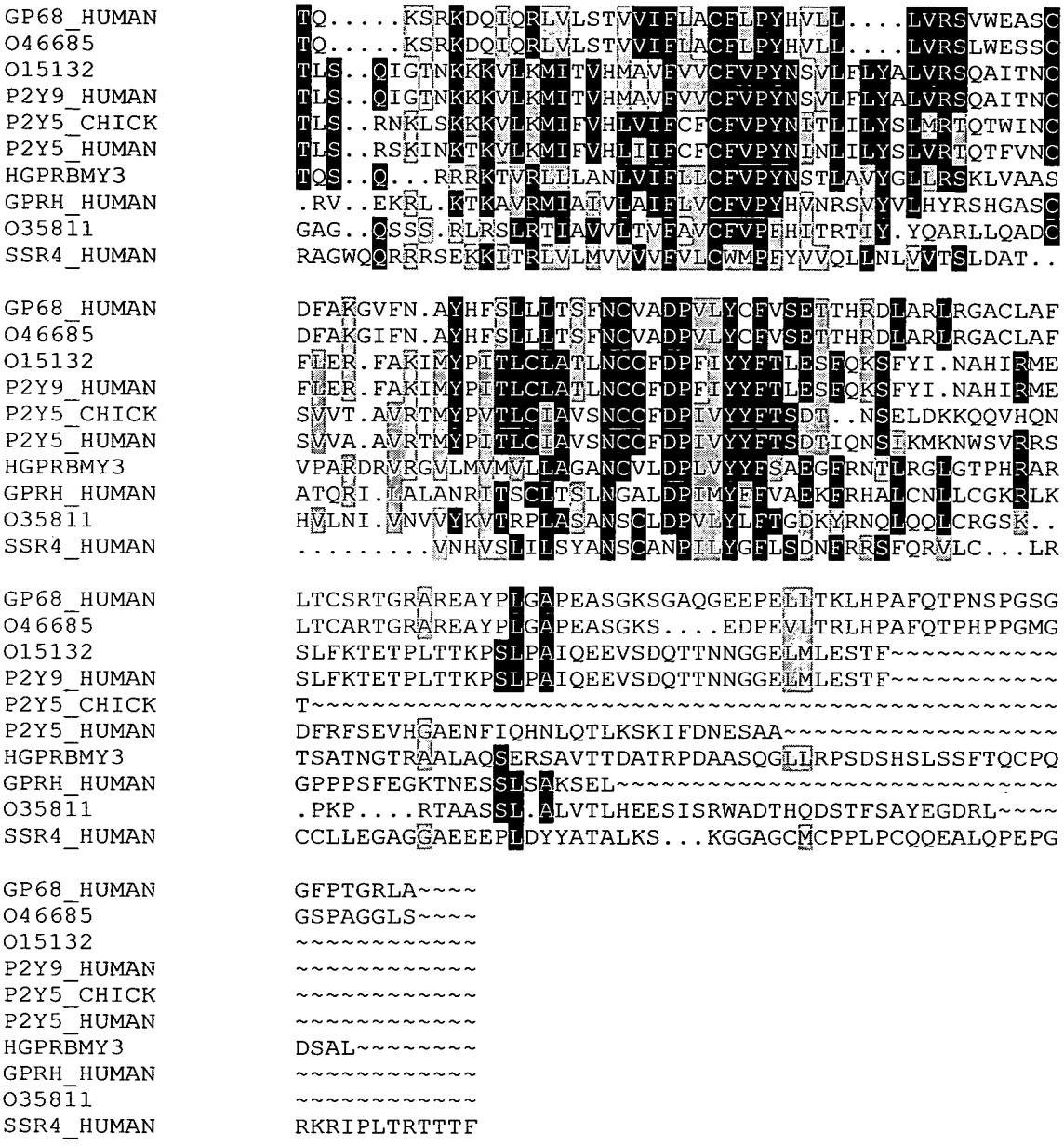

GP68_HUMAN
O46685
O15132
P2Y9_HUMAN
P2Y5_CHICK
P2Y5_HUMAN
HGPRBMY3
GPRH_HUMAN
O35811
SSR4_HUMAN

FIG. 6B



SEQUENCE	SEQ ID NO:
GP68_HUMAN	8
O46685	9
O15132	10
P2Y9_HUMAN	11
P2Y5_CHICK	12
P2Y5_HUMAN	13
HGPRBMY3	2
GPRH_HUMAN	14
O35811	15
SSR4_HUMAN	16

FIG. 7

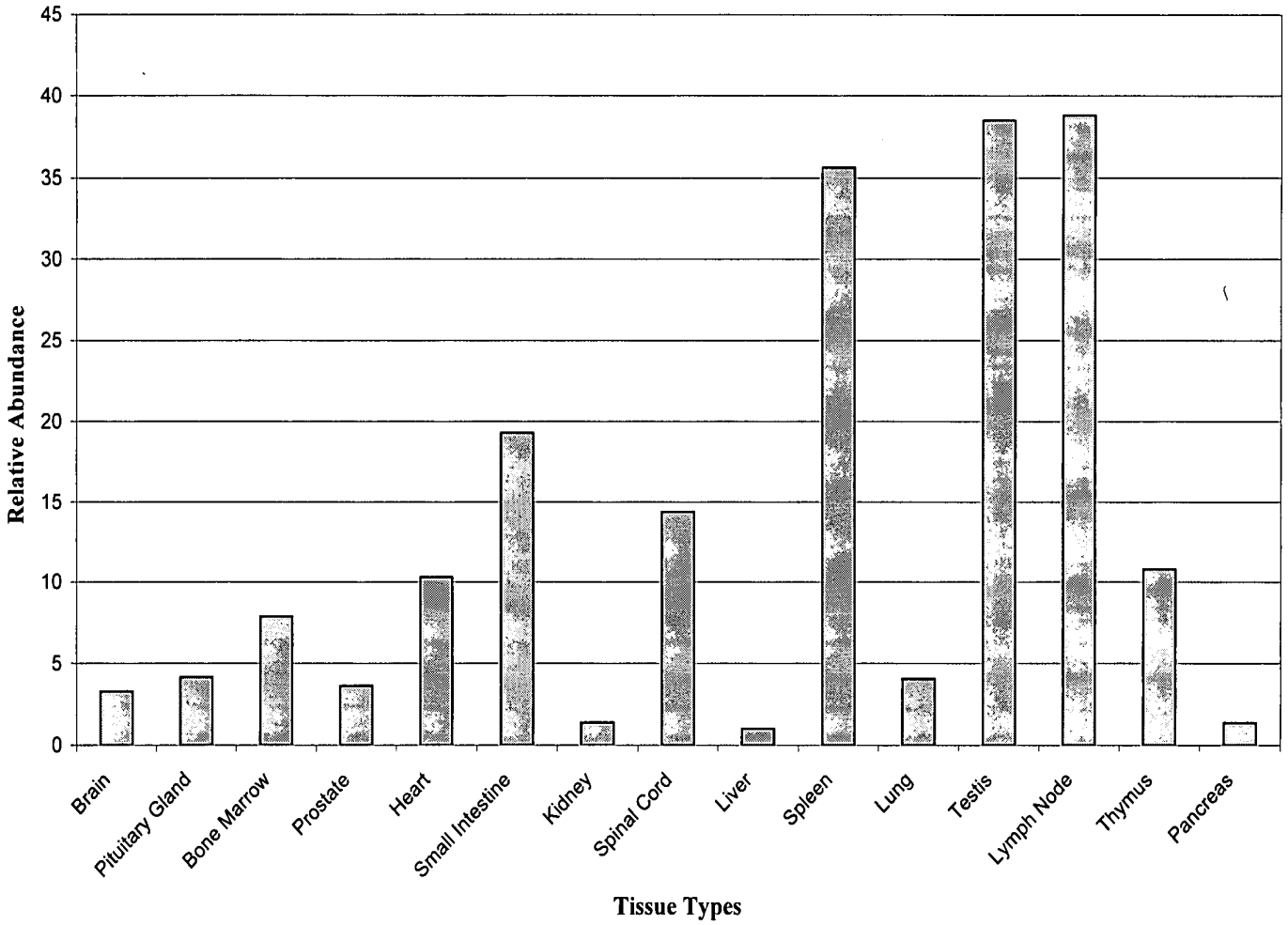

45
40
35
30
25
20
15
10
5
0
Relative Abundance
Brain
Pituitary Gland
Bone Marrow
Prostate
Heart
Small Intestine
Kidney
Spinal Cord
Liver
Spleen
Lung
Testis
Lymph Node
Thymus
Pancreas
Tissue Types

FIG. 8

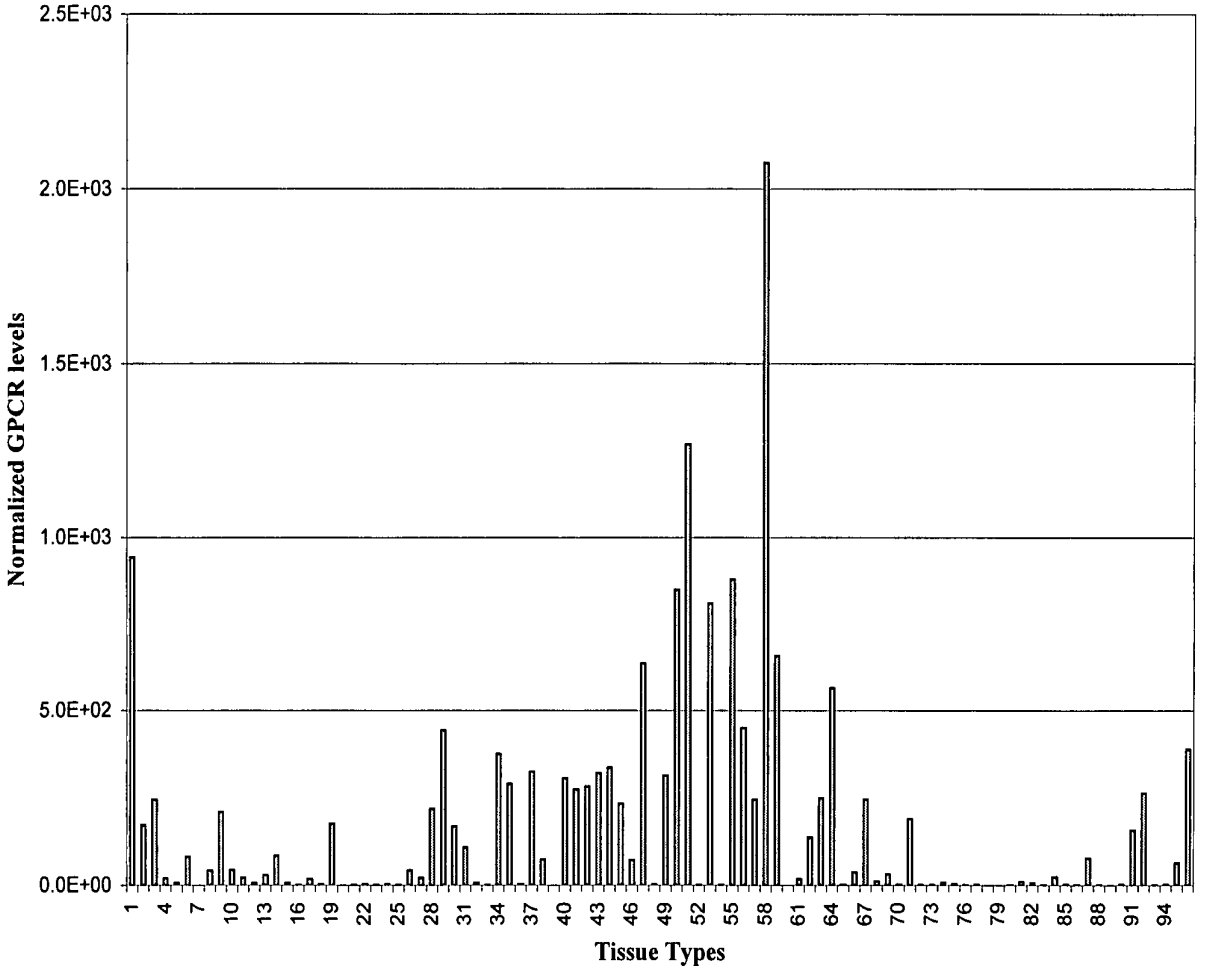

2.5E+03
2.0E+03
1.5E+03
1.0E+03
5.0E+02
0.0E+00
Normalized GPCR levels
1
4
7
10
13
16
19
22
25
28
31
34
37
40
43
46
49
52
55
58
61
64
67
70
73
76
79
82
85
88
91
94
Tissue Types

FIG. 9

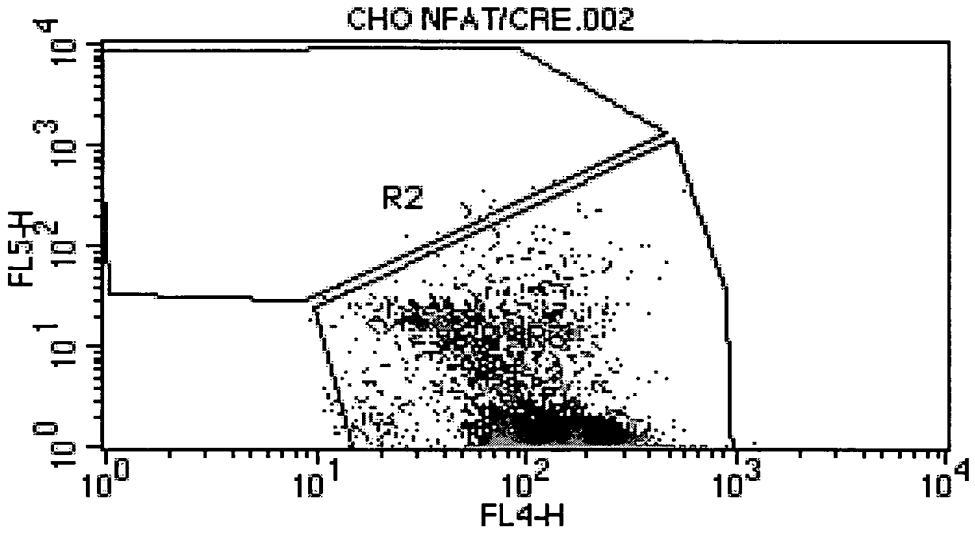

CHO NFAT/CRE.002
R2
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 10

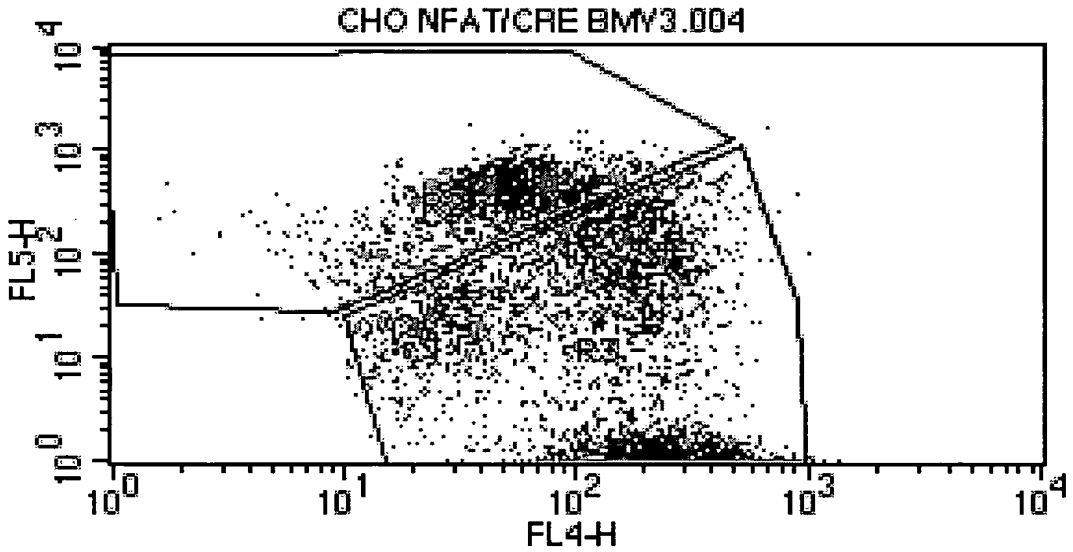

CHO NFAT/CRE BMV3.004
R2
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 11

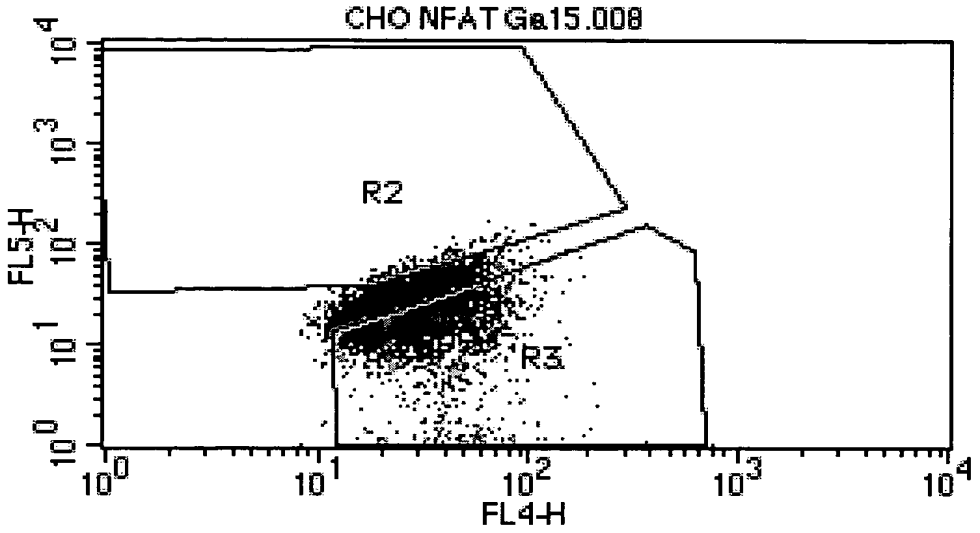

CHO NFAT Ga15.008
R2
R3
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 12

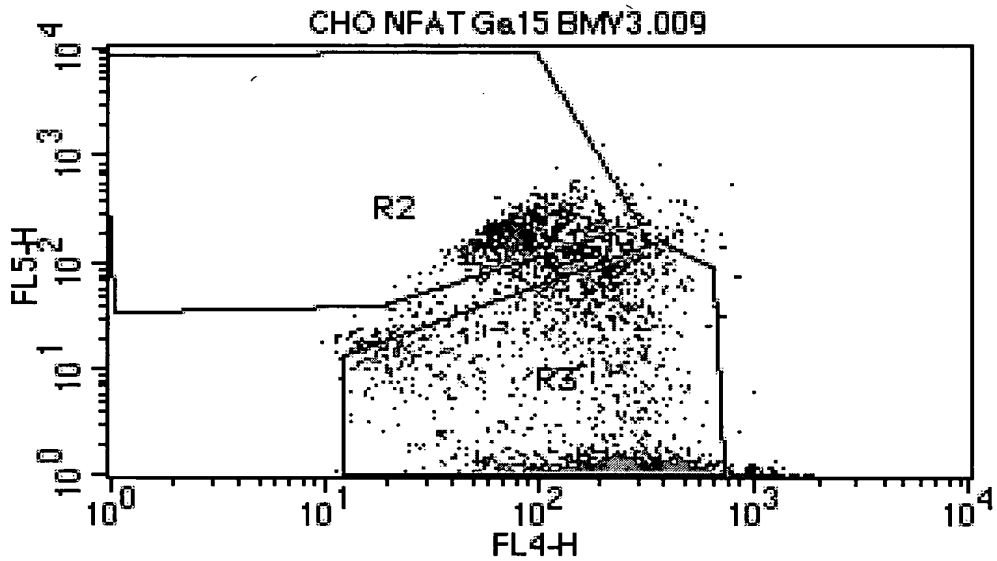

CHO NFAT Ga15 BMV3.009
R2
R3
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 13A

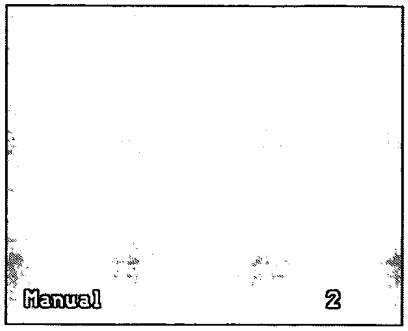


FIG. 13B

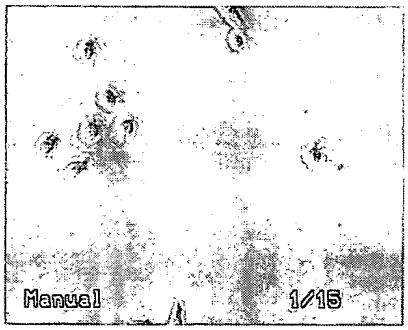


FIG. 13C

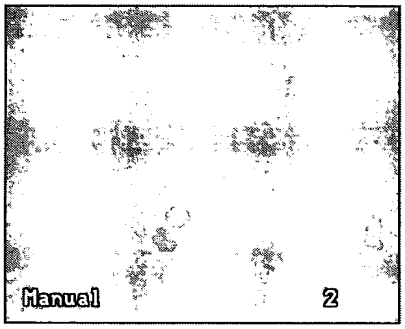


FIG. 13D

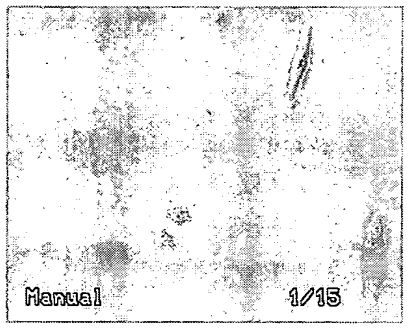


FIG. 14A

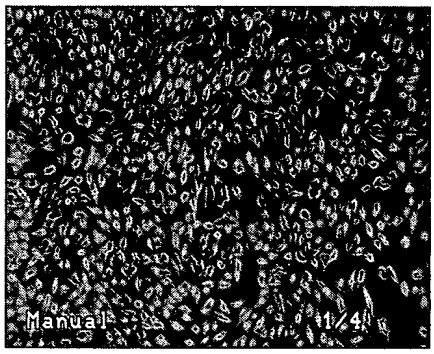


FIG. 14B

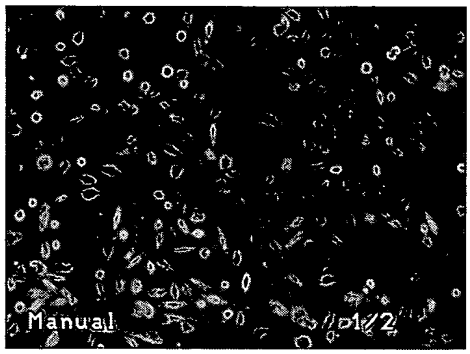


FIG. 14C

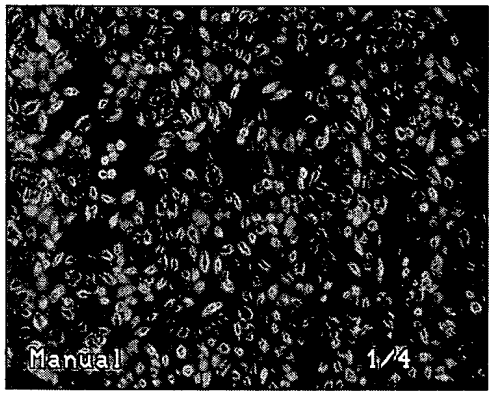


FIG. 14D

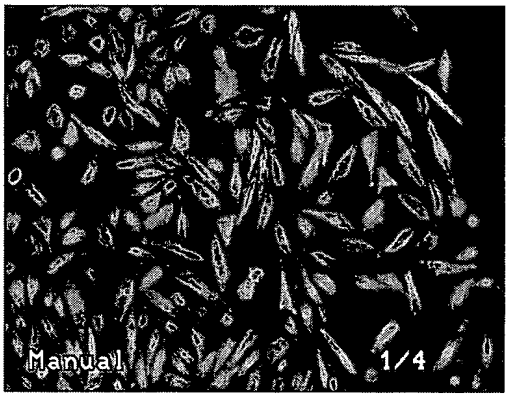


FIG. 15

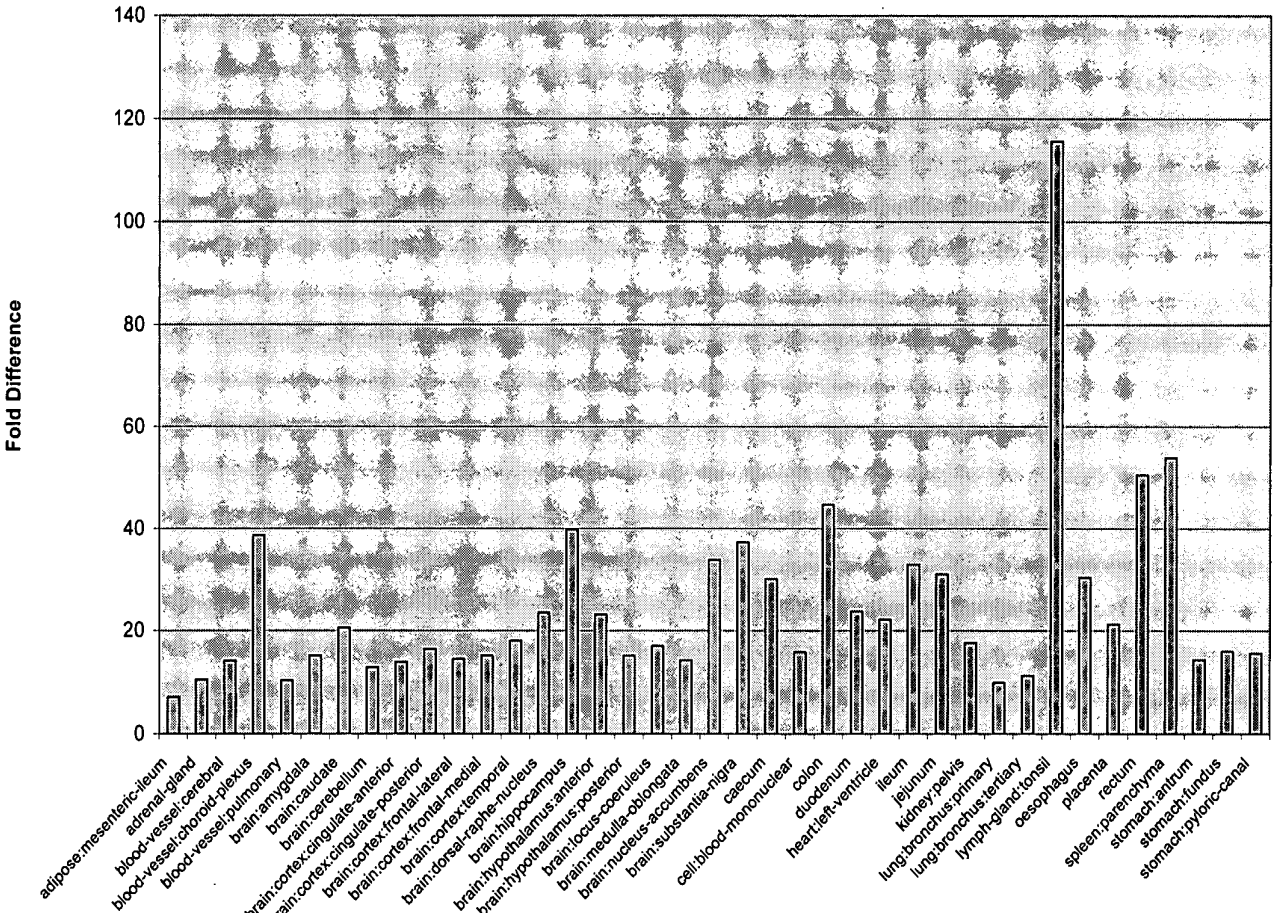
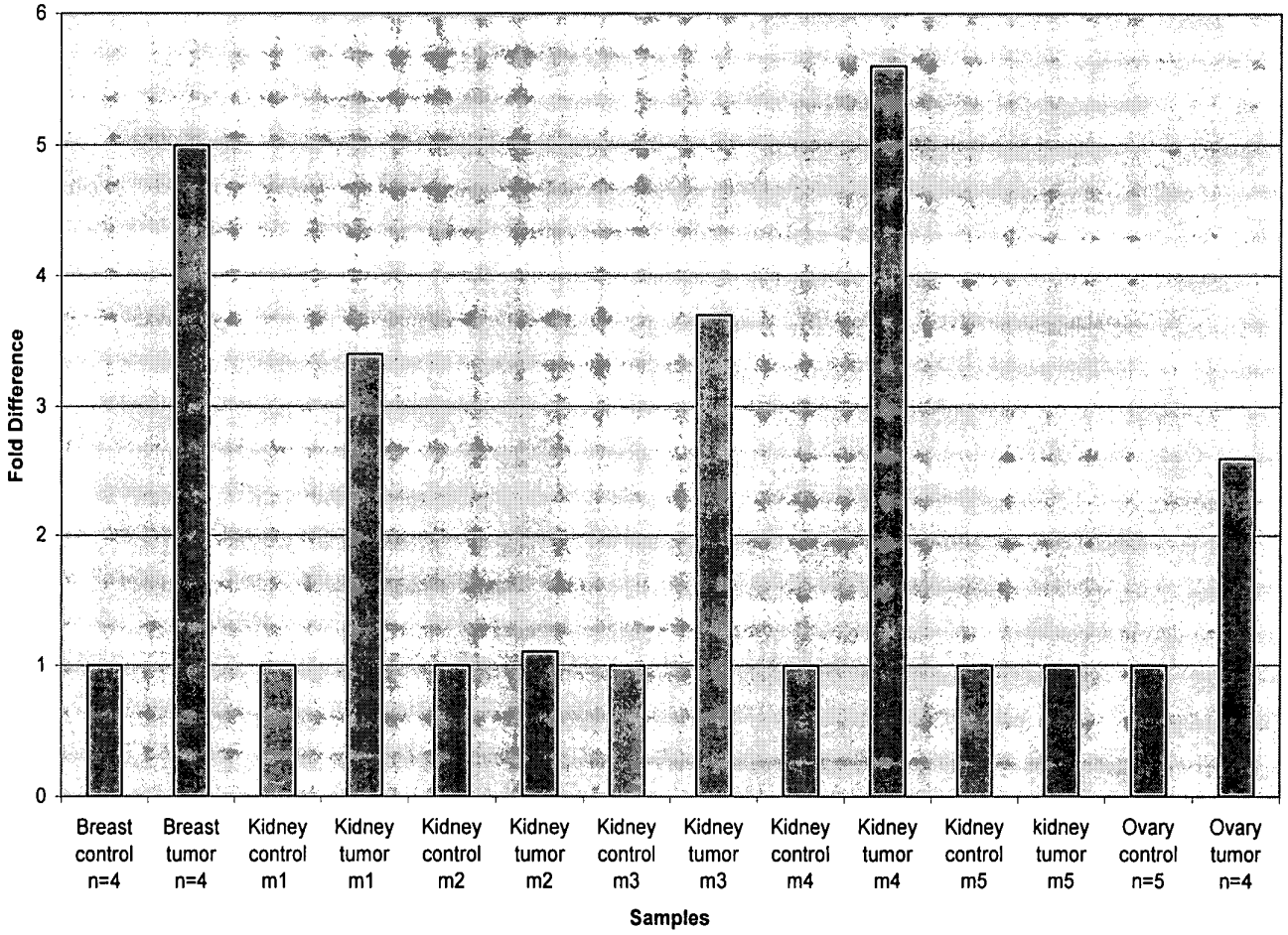

Fold Difference
140
120
100
80
60
40
20
0
adipose:mesenteric-ileum
adrenal-gland
blood-vessel:cerebral
blood-vessel:choroid-plexus
blood-vessel:pulmonary
brain:amygdala
brain:caudate
brain:cerebellum
brain:cortex:cingulate-anterior
brain:cortex:cingulate-posterior
brain:cortex:frontal-lateral
brain:cortex:frontal-medial
brain:cortex:temporal
brain:dorsal-raphe-nucleus
brain:hippocampus
brain:hypothalamus:anterior
brain:hypothalamus:posterior
brain:locus-coeruleus
brain:medulla-oblongata
brain:nucleus-accumbens
brain:substantia-nigra
caecum
cell:blood-mononuclear
colon
duodenum
heart:left-ventricle
ileum
jejunum
kidney:pelvis
lung:bronchus:primary
lung:bronchus:tertiary
lymph-gland:tonsil
oesophagus
placenta
rectum
spleen:parenchyma
stomach:antrum
stomach:fundus
stomach:pyloric-canal

FIG. 16


Fold Difference
0
1
2
3
4
5
6
Breast control n=4
Breast tumor n=4
Kidney control m1
Kidney tumor m1
Kidney control m2
Kidney tumor m2
Kidney control m3
Kidney tumor m3
Kidney control m4
Kidney tumor m4
Kidney control m5
kidney tumor m5
Ovary control n=5
Ovary tumor n=4
Samples

15/20

FIG. 17

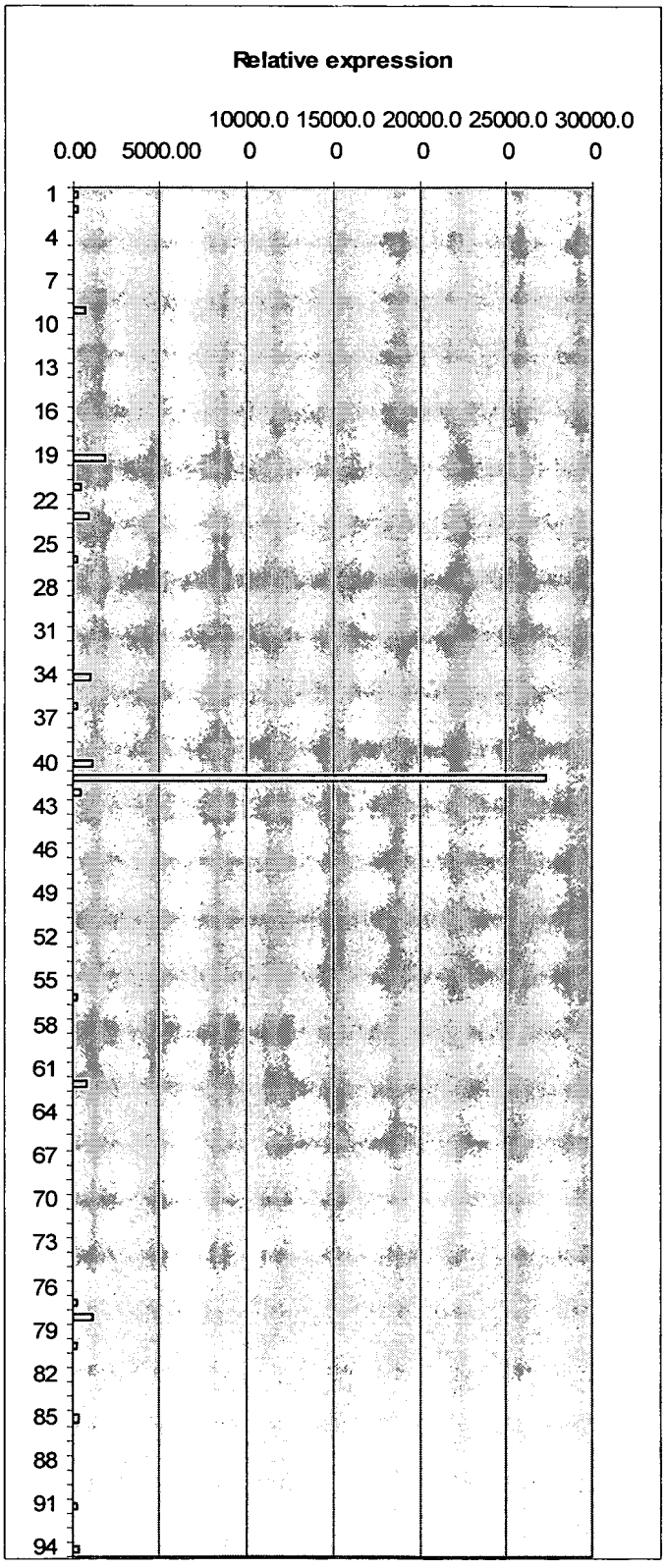

Relative expression
0.00
5000.00
10000.0
15000.0
20000.0
25000.0
30000.0
1
4
7
10
13
16
19
22
25
28
31
34
37
40
43
46
49
52
55
58
61
64
67
70
73
76
79
82
85
88
91
94

FIG. 18A

BINDER NO.	SEQUENCE	SEQ ID NO:
1	LEA**KIW**VVPAPS	17
2	TGQT**KIW**YPHST	18
3	VYS**KVWLLP**AGQ	19
4	HL**KVW**EVR**S**PG**P**	20
5	**NAKVW**TV**PS**KP**P**	21
6	**KVW**IPT**S**TWL**Q**T	22
7	**KVWSL**DISAP**Q**H	23
8	ADVLHATPSE**KVWLL**	24
9	KVV**DSN**H**KVWL**VSQT	25
10	NH**D**NTK**KVW**ILA	26
11	**KLWIL**ADNFTNR	35
12	INSPHELK**KLWLLP**P	36
13	FPH**KLWVLP**VKT	37
14	**KLWT**I**P**SNDYP**P**	38
15	**KLWEL**YP**T**V**P**AG	39
16	**KLW**IPHTSQ**P**FL	40
17	**KLWD**I**TA**PL**P**K**P**	41
18	NA**KLWQ**I**PA**I**P**H	42
19	**KLW**VPQNR**P**ELV	43
20	**KLWEL**YP**T**V**P**AG	44
21	TS**TPHRVW**QL**P**V	45
22	**TTPHRVW**NL**P**LEAQQ	46

FIG. 18B

BINDER NO.	SEQUENCE	SEQ ID NO:
1	L E A K I W V V P A P S	17
	TTG GAG GCG AAG ATT TGG GTG GTG CCT GCG CCT TCT	47
	CTX GAO GCX AAO ATB TGG GTX GTX CCX GCX CCX TCX	78
	TTO AGZ	
2	T G Q T K I W Y P H S T	18
	ACT GGG CAG ACT AAG ATT TGG TAT CCG CAT TCT ACG	48
	GCX GGX CAO ACX AAO ATB TGG TAZ CCX CAZ TCX ACX	79
	AGZ	
3	V Y S K V W L L P A G Q	19
	GTT TAT TCG AAG GTT TGG CTG CTT CCG GCG GGT CAG	49
	GTX TAZ TCX AAO GTX TGG CTX CTX CCX GCX GGX CAO	80
	AGZ CTO CTO	
4	H L K V W E V R S P G P	20
	CAT CTT AAG GTG TGG GAG GTT CGG TCG CCT GGG CCT	50
	CAZ CTX AAO GTX TGG GAO GTX CGX TCX CCX GGX CCX	81
	TTO AGO AGZ	
5	N A K V W T V P S K P P	21
	AAT GCG AAG GTG TGG ACG GTT CCG TCG AAG CCG CCT	51
	AAZ GCX AAO GTX TGG ACX GTX CCX TCX AAO CCX CCX	82
	AGZ	
6	K V W I P T S T W L Q T	22
	AAG GTG TGG ATT CCT ACG AGT ACT TGG CTG CAG ACT	52
	AAO GTX TGG ATB CCX ACX TCX ACX TGG CTX CAO ACX	83
	AGZ TTO	
7	K V W S L D I S A P Q H	23
	AAG GTT TGG AGT TTG GAT ATT TCG GCT CCG CAG CAT	53
	AAO GTX TGG TCX CTX GAZ ATB TCX GCX CCX CAO CAZ	84
	AGX TTO AGZ	
8	A D V L H A T P S E K V W L L	24
	GCG GAT GTG TTG CAT GCA TAC CCC TCT GAG AAG GTC TGG CTT CTG	54
	GCX GAZ GTX CTX CAZ GCX ACX CCX TCX GAO AAO GTX TGG CTX CTX	85
	TTO AGZ TTO TTO	
9	K V V D S N H K V W L V S Q T	25
	AAG GTG GTG GAT AGT AAT CAT AAG GTT TGG CTG GTT TCT CAG ACT	55
	AAO GTX GTX GAZ TCX AAZ CAZ AAO GTX TGG CTX GTX TCX CAO ACX	86
	AGZ TTO AGZ	
10	N H D N T K K V W I L A	26
	AAT CAT GAT AAT ACT AAG AAG GTT TGG ATT CTG GCT	56
	AAZ CAZ GAZ AAZ ACX AAO AAO GTX TGG ATB CTX GCX	87
	TTO	
11	K L W I L A D N F T N R	35
	AAG CTT TGG ATT CTG GCT GAT AAT TTT ACG AAT CGG	57
	AAO CTX TGG ATB CTX GCX GAZ AAZ TTZ ACX AAZ CGX	88
	TTO TTO AGO	

FIG. 18C

BINDER NO.	SEQUENCE	SEQ ID NO:
12	I N S P H E L K K L W L L P P	36
	ATT AAT TCT CCG CAT GAA CTT AAG AAG CTG TGG CTT CTG CCG CCT	57
	ATB AAZ TCX CCX CAZ GAO CTX AAO AAO CTX TGG CTX CTX CCX CCX	89
	AGX TTO TTO TTO TTO	
13	F P H K L W V L P V K T	37
	TTT CCG CAT AAG TTG TGG GTT TTG CCG GTG AAG ACT	58
	TTZ CCX CAZ AAO CTX TGG GTX CTX CCX GTX AAO ACX	90
	TTO TTO	
14	K L W T I P S N D Y P P	38
	AAG CTG TGG ACG ATT CCT AGT AAT GAT TAT CCG CCT	59
	AAO CTX TGG ACX ATB CCX TCX AAZ GAZ TAZ CCX CCX	91
	TTO AGZ	
15	K L W E L Y P T V P A G	39
	AAG CTT TGG GAG TTG TAT CCG ACT GTG CCG GCT GGT	60
	AAO CTX TGG GAO CTX TAZ CCX ACX GTX CCX GCX GGX	92
	TTO TTO	
16	K L W I P H T S Q P F L	40
	AAG CTG TGG ATT CCT CAT ACT TCT CAG CCG TTT CTT	61
	AAO CTX TGG ATB CCX CAZ ACX TCX CAO CCX TTZ CTX	93
	TTO AGZ TTO	
17	K L W D I T A P L P K P	41
	AAG TTG TGG GAT ATT ACG GCT CCT TTG CCT AAG CCT	62
	AAO CTX TGG GAZ ATB ACX GCX CCX CTX CCX AAO CCX	94
	TTO TTO	
18	N A K L W Q I P A I P H	42
	AAT GCG AAG CTT TGG TAG ATT CCT GCG ATT CCG CAT	63
	AAZ GCX AAO CTX TGG CAO ATB CCX GCX ATB CCX CAZ	95
	TTO	
19	K L W V P Q N R P E L V	43
	AAG CTT TGG GTT CCG CAG AAT CGT CCG GAG CTG GTG	67
	AAO CTX TGG GTX CCX CAO AAZ CGX CCX GAO CTX GTX	96
	TTO AGO TTO	
20	K L W E L Y P T V P A G	44
	AAG CTT TGG GAG TTG TAT CCG ACT GTG CCG GCT GGT	68
	AAO CTX TGG GAO CTX TAZ CCX ACX GTX CCX GCX GGX	97
	TTO TTO	
21	T S T P H R V W Q L P V	45
	ACT TCT ACT CCT CAT AGG GTT TGG CAG CTG CCT GTT	69
	ACX TCX ACX CCX CAZ CGX GTX TGG CAO CTX CCX GTX	98
	AGZ AGO TTO	
22	T T P H R V W N L P L E A Q Q	46
	ACT ACT CCT CAT CGT GTA TGG AAC CTG CCC CTG GAG GCT CAG CAG	70
	ACX ACX CCX CAZ CGX GTX TGG AAZ CTX CCX CTX GAO GCX CAO CAO	99
	AGO TTO TTO	

FIG. 19A

GPC RECEPTOR	BINDER SEQUENCE	SEQ ID NO:
HGPRBMY11	THGFGHRVWSVPLRS	73
HGPRBMY23	SRVSGAKVWFLSNWS	74
P2Y10	AMNSHKIWMLPH	75
P2Y10	GLKIWSLPPHHG	76
P2Y10	KVWQMAPTTAFS	77

FIG. 19B

GPC RECEPTOR	BINDER SEQUENCE														SEQ ID NO:
HGPRBMY11	T	H	G	F	G	H	R	V	W	S	V	P	L	R	S	73
	ACT	CAT	GGT	TTT	GGT	CAT	CGT	GTG	TGG	AGT	GTT	CCG	TTG	CGT	TCG	100
	ACX	CAZ	GGX	TTZ	GGX	CAZ	CGX	GTX	TGG	TCX	GTX	CCX	CTX	CGX	TCX	105
							AGO			AGZ			TTO	AGO	AGZ	
HGPRBMY23	S	R	V	S	G	A	K	V	W	F	L	S	N	W	S	74
	AGT	AGG	GTG	TCT	GGT	GCG	AAG	GTT	TGG	TTT	TTG	AGT	AAT	TGG	TCT	101
	TCX	CGX	GTX	TCX	GGX	GCX	AAO	GTX	TGG	TTZ	CTX	TCX	AAZ	TGG	TCX	106
	AGZ	AGO		AGZ							TTO	AGZ			AGZ	
P2Y10	A	M	N	S	H	K	I	W	M	L	P	H				75
	GCT	ATG	AAT	AGT	CAT	AAG	ATT	TGG	ATG	TTG	CCG	CAT				102
	GCX	ATG	AAZ	TCX	CAZ	AAO	ATB	TGG	ATG	CTX	CCX	CAZ				107
				AGZ						TTO						
P2Y10	G	L	K	I	W	S	L	P	P	H	H	G				76
	GGT	CTG	AAG	ATT	TGG	AGT	TTG	CCG	CCG	CAT	CAT	GGG				103
	GGX	CTX	AAO	ATB	TGG	TCX	CTX	CCX	CCX	CAZ	CAZ	GGX				108
		TTO				AGZ	TTO									
P2Y10	K	V	W	Q	M	A	P	T	T	A	F	S				77
	AAG	GTT	TGG	TAG	ATG	GCG	CCT	ACG	ACT	GCG	TTT	TCG				104
	AAO	GTX	TGG	CAO	ATG	GCX	CCX	ACX	ACX	GCX	TTZ	TCX				109
												AGZ				

FIG. 20

HGPRBMY11

MEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLFISTL
PFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFRLLHVTSIRSAWILCGIIWILI
MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVS
HRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL
KSALRKGHPQKAKTKCVFPVSVWLRKETRV (SEQ ID NO:110)

HGPRBMY23

MNEPLDYLANASDFPDYAAAFGNCTDENIPLKMHYLPVIYGIIFLVGFPGNAVVISTYIFKMRPWKSSTIIMLNL
ACTDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIHPMSCFSIHKTRCA
VVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIKWYNLILTATTFCLPLVIVTLCYTTIIHTL
THGLQTDSCLKQKARRLTILLLLAFYVCFLPFHILRVIRIESRLLSISCSIENQIHEAYIVSRPLAALNTFGNLL
LYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYSNNP (SEQ ID NO:111)

P2Y10

MANLDKYTETFKMGSNSTSTAEIYCNVTNVKFQYSLYATTYILIFIPGLLANSAALWVLCRFISKKNKAIIFMIN
LSVADLAHVLSLPLRIYYYISHHWPFQRALCLLCFYLKYLNMYASICFLTCISLQRCFFLLKPFRARDWKRRYDV
GISAAIWIVVGTACLPFPILRSTDLNNNKSCFADLGYKQMNAVALVGMITVAELAGFVIPVIIIAWCTWKTTISL
RQPPMAFQGISERQKALRMVFMCAAVFFICFTPYHINFIFYTMVKETIISSCPVVRIALYFHPFCLCLASLCCLL
DPILYYFMASEFRDQLSRHGSSVTRSRLMSKESGSSMIG (SEQ ID NO:112)